

CERTIFICATE OF EXPRESS MAIL
EXPRESS MAILING NO.: EL611000475US
DATE OF DEPOSIT: February 13, 2001

PATENT

IN THE UNITED STATES PATENT AND TRADEMARK OFFICE

In re Application of:

R. Sanders Williams and
Beverly Rothermel

Serial No.: Unknown

Filed: February 13, 2001

For: METHODS AND COMPOSITIONS
RELATING TO MUSCLE SELECTIVE
CALCINEURIN INTERACTING
PROTEIN (MCIP)

Group Art Unit: Unknown

Examiner: Unknown

Atty. Dkt. No.: UTSD:674US

STATEMENT AS REQUIRED UNDER 37 C.F.R. § 1.821(f)

BOX SEQUENCE

Commissioner for Patents
Washington, D.C. 20231

Commissioner:

Submitted herewith is a computer readable form and a paper copy of the sequence listing of those sequences in the captioned patent application. The computer readable form of the sequence listing is the same as the paper copy of the sequence listing. The sequence information provided in the Specification is also the same as the sequence listing of the enclosed computer readable and paper forms of the sequence listing.

Respectfully submitted,



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Reg. No. 37,642
Attorney for Applicants

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Date: February 13, 2001

SEQUENCE LISTING

<110> WILLIAMS, R. SANDERS
ROTHERMEL, BEVERLY

<120> METHODS AND COMPOSITIONS RELATING TO MUSCLE SELECTIVE
CALCINEURIN INTERACTING PROTEIN (MCIP)

<130> UTSD:674US

<140> UNKNOWN

<141> 2001-02-13

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<151> 2000-07-07

<160> 27

<170> PatentIn Ver. 2.1

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His Leu Asp Pro Arg Val Phe Val Asp Gly Leu Cys Arg Ala Lys Phe
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Ala Pro Pro Asn Pro Asp Lys Gln Phe Leu Ile Ser Pro Pro Ala Ser
 100 105 110

Pro Pro Val Gly Trp Lys Gln Val Glu Asp Ala Thr Pro Val Ile Asn
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Lys Ser Phe Lys Arg Val Arg Ile Asn Phe Ser Asn Pro Leu Ser Ala
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Ala Asp Ala Arg Leu Arg Leu His Lys Thr Glu Phe Leu Gly Lys Glu
 65 70 75 80

Met Lys Leu Tyr Phe Ala Gln Thr Leu His Ile Gly Ser Ser His Leu
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100 105 110

Pro Pro Val Gly Trp Lys Gln Val Glu Asp Ala Thr Pro Val Ile Asn
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Tyr Asp Leu Leu Tyr Ala Ile Ser Lys Leu Gly Pro Gly Glu Lys Tyr
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Cys Glu Ser Asp Gln Glu Asn Glu Glu Glu Glu Glu Met Glu Arg
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Ala Asp Ala Arg Leu Arg Leu His Lys Thr Glu Phe Leu Gly Lys Glu
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Met Lys Leu Tyr Phe Ala Gln Thr Leu His Ile Gly Ser Ser His Leu
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Ala Pro Pro Asn Pro Asp Lys Gln Phe Leu Ile Ser Pro Pro Ala Ser
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Pro Pro Val Gly Trp Lys Gln Val Glu Asp Ala Thr Pro Val Ile Asn

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Lys Ser Phe Lys Arg Val Arg Ile Asn Phe Ser Asn Pro Leu Ser Ala
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Ala Pro Pro Asn Pro Asp Lys Gln Phe Leu Ile Ser Pro Pro Ala Ser
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Pro Pro Val Gly Trp Lys Gln Val Glu Asp Ala Thr Pro Val Ile Asn
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Glu Leu His Ala Ala Thr Asp Pro Thr Pro Ser Val Val Val His Val
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Cys Glu Ser Asp Gln Glu Asn Glu Glu Glu Glu Met Glu Arg
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Leu Lys Leu Tyr Phe Ala Gln Val Gln Thr Pro Glu Thr Asp Gly Asp
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Val Val His Val Cys Asp Ser Asp Met Glu Glu Glu Asp Pro Lys
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Leu Lys Leu Tyr Phe Ala Gln Val Gln Thr Pro Glu Thr Asp Gly Asp
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Lys Leu His Leu Ala Pro Pro Gln Pro Ala Lys Gln Phe Leu Ile Ser
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Pro Pro Ser Ser Pro Pro Val Gly Trp Lys Pro Ile Ser Asp Ala Thr
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Pro Val Leu Asn Tyr Asp Leu Leu Tyr Ala Val Ala Lys Leu Gly Pro
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145 150 155 160

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Pro Ser Val Ser Asn

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 Lys Ser Phe Arg Arg Val Arg Ile Asn Phe Ser His Pro Lys Ser Ala
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 85 90 95
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 Pro Pro Ser Ser Pro Pro Val Gly Trp Lys Pro Ile Ser Asp Ala Thr
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Glu Thr Arg Ala Lys Phe Glu Ser Leu Phe Arg Thr Tyr Asp Lys Asp

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Ile Thr Phe Gln Tyr Phe Lys Ser Phe Lys Arg Val Arg Ile Asn Phe

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Ile Gly Ser Ser His Leu Ala Pro Pro Asn Pro Asp Lys Gln Phe Leu

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Glu Ser Leu Phe Arg Thr Tyr Asp Lys Asp Ile Thr Phe Gln Tyr Phe
 35 40 45

Lys Ser Phe Lys Arg Val Arg Ile Asn Phe Ser Asn Pro Phe Ser Ala
 50 55 60

Ala Asp Ala Arg Leu Gln Leu His Lys Thr Glu Phe Leu Gly Lys Glu
 65 70 75 80

Met Lys Leu Tyr Phe Ala Gln Thr Leu His Ile Gly Ser Ser His Leu
 85 90 95

Ala Pro Pro Asn Pro Asp Lys Gln Phe Leu Ile Ser Pro Pro Ala Ser
 100 105 110

Pro Pro Val Gly Trp Lys Gln Val Glu Asp Ala Thr Pro Val Ile Asn
 115 120 125

Tyr Asp Leu Leu Tyr Ala Ile Ser Lys Leu Gly Pro Gly Glu Lys Tyr
 130 135 140

Glu Leu His Ala Ala Thr Asp Thr Thr Pro Ser Val Val Val His Val
 145 150 155 160

Cys Glu Ser Asp Gln Glu Lys Glu Glu Glu Glu Met Glu Arg Met
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Arg Arg Pro Lys Pro Lys Ile Ile Gln Thr Arg Arg Pro Glu Tyr Thr
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Pro Ile His Leu Ser
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 Met Glu Glu Val Asp Leu Gln Asp Leu
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ccc agc gcc acc atc gcc tgt cac ctg gac ccg cgc gtg ttc gtg gac
 Pro Ser Ala Thr Ile Ala Cys His Leu Asp Pro Arg Val Phe Val Asp
 10 15 20 25

ggc ctg tgc cgg gcc aaa ttt gag tcc ctc ttt agg acg tat gac aag
 Gly Leu Cys Arg Ala Lys Phe Glu Ser Leu Phe Arg Thr Tyr Asp Lys
 30 35 40

gac atc acc ttt cag tat ttt aag agc ttc aaa cga gtc aga ata aac	195		
Asp Ile Thr Phe Gln Tyr Phe Lys Ser Phe Lys Arg Val Arg Ile Asn			
45	50	55	
ttc agc aac ccc ttc tcc gca gca gat gcc agg ctc cag ctg cat aag	243		
Phe Ser Asn Pro Phe Ser Ala Ala Asp Ala Arg Leu Gln Leu His Lys			
60	65	70	
act gag ttt ctg gga aag gaa atg aag tta tat ttt gct cag acc tta	291		
Thr Glu Phe Leu Gly Lys Glu Met Lys Leu Tyr Phe Ala Gln Thr Leu			
75	80	85	
cac ata gga agc tca cac ctg gct ccg cca aat cca gac aag cag ttt	339		
His Ile Gly Ser Ser His Leu Ala Pro Pro Asn Pro Asp Lys Gln Phe			
90	95	100	105
ctg atc tcc cct ccc gcc tct ccg cca gtg gga tgg aaa caa gtg gaa	387		
Leu Ile Ser Pro Pro Ala Ser Pro Pro Val Gly Trp Lys Gln Val Glu			
110	115	120	
gat gcg acc cca gtc ata aac tat gat ctc tta tat gcc atc tcc aag	435		
Asp Ala Thr Pro Val Ile Asn Tyr Asp Leu Leu Tyr Ala Ile Ser Lys			
125	130	135	
ctg ggg cca ggg gaa aag tat gaa ttg cac gca gcg act gac acc act	483		
Leu Gly Pro Gly Glu Lys Tyr Glu Leu His Ala Ala Thr Asp Thr Thr			
140	145	150	
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Pro Ser Val Val Val His Val Cys Glu Ser Asp Gln Glu Lys Glu Glu			
155	160	165	
gaa gag gaa atg gaa aga atg agg aga cct aag cca aaa att atc cag	579		
Glu Glu Glu Met Glu Arg Met Arg Arg Pro Lys Pro Lys Ile Ile Gln			
170	175	180	185
acc agg agg ccg gag tac acg ccg atc cac ctc agc tgaactggca	625		
Thr Arg Arg Pro Glu Tyr Thr Pro Ile His Leu Ser			
190	195		
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tgcagagagg ttgtgaaaac agcagcaatg caatgtggaa attgttagcgt ttcctttctt	1105		

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His Leu Asp Pro Arg Val Phe Val Asp Gly Leu Cys Arg Ala Lys Phe
20 25 30

Glu Ser Leu Phe Arg Thr Tyr Asp Lys Asp Ile Thr Phe Gln Tyr Phe
35 40 45

Lys Ser Phe Lys Arg Val Arg Ile Asn Phe Ser Asn Pro Phe Ser Ala
50 55 60

Ala Asp Ala Arg Leu Gln Leu His Lys Thr Glu Phe Leu Gly Lys Glu
65 70 75 80
Met Lys Leu Tyr Phe Ala Gln Thr Leu His Ile Gly Ser Ser His Leu
85 90 95
Ala Pro Pro Asn Pro Asp Lys Gln Phe Leu Ile Ser Pro Pro Ala Ser
100 105 110
Pro Pro Val Gly Trp Lys Gln Val Glu Asp Ala Thr Pro Val Ile Asn
115 120 125
Tyr Asp Leu Leu Tyr Ala Ile Ser Lys Leu Gly Pro Gly Glu Lys Tyr
130 135 140
Glu Leu His Ala Ala Thr Asp Thr Pro Ser Val Val Val His Val
145 150 155 160
Cys Glu Ser Asp Gln Glu Lys Glu Glu Glu Met Glu Arg Met
165 170 175
Arg Arg Pro Lys Pro Lys Ile Ile Gln Thr Arg Arg Pro Glu Tyr Thr
180 185 190
Pro Ile His Leu Ser
195

<210> 16
<211> 197
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Met Glu Glu Val Asp Leu Gln Asp Leu Pro Ser Ala Thr Ile Ala Cys
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His Leu Asp Pro Arg Val Phe Val Asp Gly Leu Cys Arg Ala Lys Phe
20 25 30

Glu Ser Leu Phe Arg Thr Tyr Asp Lys Asp Ile Thr Phe Gln Tyr Phe
35 40 45

Lys Ser Phe Lys Arg Val Arg Ile Asn Phe Ser Asn Pro Phe Ser Ala
50 55 60

Ala Asp Ala Arg Leu Gln Leu His Lys Thr Glu Phe Leu Gly Lys Glu
65 70 75 80

Met Lys Leu Tyr Phe Ala Gln Thr Leu His Ile Gly Ser Ser His Leu
85 90 95

Ala Pro Pro Asn Pro Asp Lys Gln Phe Leu Ile Ser Pro Pro Ala Ser
100 105 110

Pro Pro Val Gly Trp Lys Gln Val Glu Asp Ala Thr Pro Val Ile Asn

115	120	125
Tyr Asp Leu Leu Tyr Ala Ile Ser Lys Leu Gly Pro Gly Glu Lys Tyr		
130	135	140
Glu Leu His Ala Ala Thr Asp Thr Thr Pro Ser Val Val Val His Val		
145	150	155
160		
Cys Glu Ser Asp Gln Glu Lys Glu Glu Glu Glu Met Glu Arg Met		
165	170	175
Arg Arg Pro Lys Pro Lys Ile Ile Gln Thr Arg Arg Pro Glu Tyr Thr		
180	185	190
Pro Ile His Leu Ser		
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gaagggggaa tgccagcccc tagc atg gac tgt gat gtt tcc act ctg gtt 231		
Met Asp Cys Asp Val Ser Thr Leu Val		
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gcc tgt gtg gat gtc gag gtc ttt acc aat cag gag gtt aag gaa 279		
Ala Cys Val Val Asp Val Glu Val Phe Thr Asn Gln Glu Val Lys Glu		
10	15	20
25		
aaa ttt ggg gga ctg ttt cgg act tat gat gac tgt gtg acg ttc cag 327		
Lys Phe Gly Gly Leu Phe Arg Thr Tyr Asp Asp Cys Val Thr Phe Gln		
30	35	40
cta ttt aag agt ttc aga cgt gtc cgt ata aac ttc agc aat cct aaa 375		
Leu Phe Lys Ser Phe Arg Arg Val Arg Ile Asn Phe Ser Asn Pro Lys		
45	50	55
tct gca gcc cga gct agg ata gag ctt cat gaa acc caa ttc aga ggg 423		
Ser Ala Ala Arg Ala Arg Ile Glu Leu His Glu Thr Gln Phe Arg Gly		
60	65	70
aaa aaa tta aag ctc tac ttt gca cag gtt cag act cca gag aca gat 471		
Lys Lys Leu Lys Leu Tyr Phe Ala Gln Val Gln Thr Pro Glu Thr Asp		
75	80	85

gga gac aaa ctg cac ttg gct cca ccc cag cct gcc aaa cag ttt ctc	519
Gly Asp Lys Leu His Leu Ala Pro Pro Gln Pro Ala Lys Gln Phe Leu	
90 95 100 105	
atc tcg ccc cct tcc tcc cca cct gtt agc tgg cag ccc atc aac gat	567
Ile Ser Pro Pro Ser Ser Pro Pro Val Ser Trp Gln Pro Ile Asn Asp	
110 115 120	
gcc acg cca gtc ctc aac tat gac ctc ctc tat gct gtg gcc aaa cta	615
Ala Thr Pro Val Leu Asn Tyr Asp Leu Leu Tyr Ala Val Ala Lys Leu	
125 130 135	
gga cca gga gag aag tat gag ctc cat gca ggg act gag tcc acc cca	663
Gly Pro Gly Glu Lys Tyr Glu Leu His Ala Gly Thr Glu Ser Thr Pro	
140 145 150	
agt gtc gtc gtg cac gtg tgc gac agt gac ata gag gaa gag gag	711
Ser Val Val Val His Val Cys Asp Ser Asp Ile Glu Glu Glu Glu Asp	
155 160 165	
cca aag act tcc cca aag cca aaa atc atc caa act cgg cgt cct ggc	759
Pro Lys Thr Ser Pro Lys Pro Lys Ile Ile Gln Thr Arg Arg Pro Gly	
170 175 180 185	
ctg cca ccc tcc gtg tcc aac tgagctgcct gctccttctc gataatagcc	810
Leu Pro Pro Ser Val Ser Asn	
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<212> PRT
<213> Homo sapiens

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Val Phe Thr Asn Gln Glu Val Lys Glu Lys Phe Gly Gly Leu Phe Arg
20 25 30

Thr Tyr Asp Asp Cys Val Thr Phe Gln Leu Phe Lys Ser Phe Arg Arg
35 40 45

Val Arg Ile Asn Phe Ser Asn Pro Lys Ser Ala Ala Arg Ala Arg Ile
50 55 60

Glu Leu His Glu Thr Gln Phe Arg Gly Lys Lys Leu Lys Leu Tyr Phe
65 70 75 80

Ala Gln Val Gln Thr Pro Glu Thr Asp Gly Asp Lys Leu His Leu Ala
85 90 95

Pro Pro Gln Pro Ala Lys Gln Phe Leu Ile Ser Pro Pro Ser Ser Pro
100 105 110

Pro Val Ser Trp Gln Pro Ile Asn Asp Ala Thr Pro Val Leu Asn Tyr
115 120 125

Asp Leu Leu Tyr Ala Val Ala Lys Leu Gly Pro Gly Glu Lys Tyr Glu
130 135 140

Leu His Ala Gly Thr Glu Ser Thr Pro Ser Val Val His Val Cys
145 150 155 160

Asp Ser Asp Ile Glu Glu Glu Asp Pro Lys Thr Ser Pro Lys Pro
165 170 175

Lys Ile Ile Gln Thr Arg Arg Pro Gly Leu Pro Pro Ser Val Ser Asn
180 185 190

<210> 19
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Met Asp Cys Asp Val Ser Thr Leu Val Ala Cys Val Val Asp Val Glu
1 5 10 15

Val Phe Thr Asn Gln Glu Val Lys Glu Lys Phe Gly Gly Leu Phe Arg
20 25 30

Thr Tyr Asp Asp Cys Val Thr Phe Gln Leu Phe Lys Ser Phe Arg Arg
35 40 45

Val Arg Ile Asn Phe Ser Asn Pro Lys Ser Ala Ala Arg Ala Arg Ile
50 55 60

Glu Leu His Glu Thr Gln Phe Arg Gly Lys Lys Leu Lys Leu Tyr Phe
65 70 75 80

Ala Gln Val Gln Thr Pro Glu Thr Asp Gly Asp Lys Leu His Leu Ala
85 90 95

Pro Pro Gln Pro Ala Lys Gln Phe Leu Ile Ser Pro Pro Ser Ser Pro
100 105 110

Pro Val Ser Trp Gln Pro Ile Asn Asp Ala Thr Pro Val Leu Asn Tyr
115 120 125

Asp Leu Leu Tyr Ala Val Ala Lys Leu Gly Pro Gly Glu Lys Tyr Glu
130 135 140

Leu His Ala Gly Thr Glu Ser Thr Pro Ser Val Val Val His Val Cys
145 150 155 160

Asp Ser Asp Ile Glu Glu Glu Asp Pro Lys Thr Ser Pro Lys Pro
165 170 175

Lys Ile Ile Gln Thr Arg Arg Pro Gly Leu Pro Pro Ser Val Ser Asn
180 185 190

<210> 20
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<212> DNA
<213> Homo sapiens

<220>
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<222> (23)..(745)

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gat agc cag tca gat ctg tgt agc act gac caa gaa gag gaa gaa gag 100
Asp Ser Gln Ser Asp Leu Cys Ser Thr Asp Gln Glu Glu Glu Glu
15 20 25

atg att ttt ggt gaa aat gaa gat gat ttg gat gag atg atg gat tta 148
Met Ile Phe Gly Glu Asn Glu Asp Asp Leu Asp Glu Met Met Asp Leu
30 35 40

agt gat ctg cct acc tca ctt ttt gct tgc agc gtc cat gaa gca gtg 196
Ser Asp Leu Pro Thr Ser Leu Phe Ala Cys Ser Val His Glu Ala Val
45 50 55

ttt gag gca cga gag cag aag gaa aga ttt gaa gca ctc ttc acc atc 244
Phe Glu Ala Arg Glu Gln Lys Glu Arg Phe Glu Ala Leu Phe Thr Ile

60

65

70

tat gat gac cag gtt act ttt cag ctg ttt aaa agc ttt aga aga gtc 292
 Tyr Asp Asp Gln Val Thr Phe Gln Leu Phe Lys Ser Phe Arg Arg Val
 75 80 85 90

aga ata aat ttc agc aaa cct gaa gcg gca gca aga gcg cga ata gaa 340
 Arg Ile Asn Phe Ser Lys Pro Glu Ala Ala Arg Ala Arg Ile Glu
 95 100 105

ctc cac gaa aca gac ttc aat ggg cag aag cta aag cta tat ttt gca 388
 Leu His Glu Thr Asp Phe Asn Gly Gln Lys Leu Lys Leu Tyr Phe Ala
 110 115 120

cag gtg cag atg tcc ggc gaa gtg cggt gac aag tcc tat ctc ctg ccg 436
 Gln Val Gln Met Ser Gly Glu Val Arg Asp Lys Ser Tyr Leu Leu Pro
 125 130 135

ccc cag cct gtc aag cag ttc ctc atc tcc cct cca gcc tct ccc cca 484
 Pro Gln Pro Val Lys Gln Phe Leu Ile Ser Pro Pro Ala Ser Pro Pro
 140 145 150

gtg ggg tgg aag cag agc gaa gat gcg atg cct gtt ata aat tat gat 532
 Val Gly Trp Lys Gln Ser Glu Asp Ala Met Pro Val Ile Asn Tyr Asp
 155 160 165 170

tta ctc tgt gct gtt tcc aaa ttg gga cca gga gag aaa tat gaa ctt 580
 Leu Leu Cys Ala Val Ser Lys Leu Gly Pro Gly Glu Lys Tyr Glu Leu
 175 180 185

cac gcg gga aca gag tcg aca ccc agc gtg gtg gtt cat gtc tgt gaa 628
 His Ala Gly Thr Glu Ser Thr Pro Ser Val Val Val His Val Cys Glu
 190 195 200

agt gaa act gaa gag gaa gag aca aaa aac ccc aaa cag aaa att 676
 Ser Glu Thr Glu Glu Glu Glu Thr Lys Asn Pro Lys Gln Lys Ile
 205 210 215

gcc cag aca agg cgc ccc gac cct ccg acc gca gcg ttg aat gag ccc 724
 Ala Gln Thr Arg Arg Pro Asp Pro Pro Thr Ala Ala Leu Asn Glu Pro
 220 225 230

cag acc ttt gat tgc gcg ctg tgaggccctt gggttgtggcg cggcgtt 775
 Gln Thr Phe Asp Cys Ala Leu
 235 240

gcccctgggtgg gctctggcca tggcgctctg tgccctgcggc cgatgcgttg ctg 828

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<211> 241

<212> PRT

<213> Homo sapiens

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Cys Ser Thr Asp Gln Glu Glu Glu Glu Met Ile Phe Gly Glu Asn
 20 25 30

Glu Asp Asp Leu Asp Glu Met Met Asp Leu Ser Asp Leu Pro Thr Ser
 35 40 45

Leu Phe Ala Cys Ser Val His Glu Ala Val Phe Glu Ala Arg Glu Gln
 50 55 60

Lys Glu Arg Phe Glu Ala Leu Phe Thr Ile Tyr Asp Asp Gln Val Thr
 65 70 75 80

Phe Gln Leu Phe Lys Ser Phe Arg Arg Val Arg Ile Asn Phe Ser Lys
 85 90 95

Pro Glu Ala Ala Ala Arg Ala Arg Ile Glu Leu His Glu Thr Asp Phe
 100 105 110

Asn Gly Gln Lys Leu Lys Leu Tyr Phe Ala Gln Val Gln Met Ser Gly
 115 120 125

Glu Val Arg Asp Lys Ser Tyr Leu Leu Pro Pro Gln Pro Val Lys Gln
 130 135 140

Phe Leu Ile Ser Pro Pro Ala Ser Pro Pro Val Gly Trp Lys Gln Ser
 145 150 155 160

Glu Asp Ala Met Pro Val Ile Asn Tyr Asp Leu Leu Cys Ala Val Ser
 165 170 175

Lys Leu Gly Pro Gly Glu Lys Tyr Glu Leu His Ala Gly Thr Glu Ser
 180 185 190

Thr Pro Ser Val Val Val His Val Cys Glu Ser Glu Thr Glu Glu Glu
 195 200 205

Glu Glu Thr Lys Asn Pro Lys Gln Lys Ile Ala Gln Thr Arg Arg Pro
 210 215 220

Asp Pro Pro Thr Ala Ala Leu Asn Glu Pro Gln Thr Phe Asp Cys Ala
 225 230 235 240

Leu

<210> 22
 <211> 241
 <212> PRT
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 20 25 30

Glu Asp Asp Leu Asp Glu Met Met Asp Leu Ser Asp Leu Pro Thr Ser
 35 40 45

Leu Phe Ala Cys Ser Val His Glu Ala Val Phe Glu Ala Arg Glu Gln
 50 55 60

Lys Glu Arg Phe Glu Ala Leu Phe Thr Ile Tyr Asp Asp Gln Val Thr
 65 70 75 80

Phe Gln Leu Phe Lys Ser Phe Arg Arg Val Arg Ile Asn Phe Ser Lys
 85 90 95

Pro Glu Ala Ala Ala Arg Ala Arg Ile Glu Leu His Glu Thr Asp Phe
 100 105 110

Asn Gly Gln Lys Leu Lys Leu Tyr Phe Ala Gln Val Gln Met Ser Gly
 115 120 125

Glu Val Arg Asp Lys Ser Tyr Leu Leu Pro Pro Gln Pro Val Lys Gln
 130 135 140

Phe Leu Ile Ser Pro Pro Ala Ser Pro Pro Val Gly Trp Lys Gln Ser
 145 150 155 160

Glu Asp Ala Met Pro Val Ile Asn Tyr Asp Leu Leu Cys Ala Val Ser
 165 170 175

Lys Leu Gly Pro Gly Glu Lys Tyr Glu Leu His Ala Gly Thr Glu Ser
 180 185 190

Thr Pro Ser Val Val Val His Val Cys Glu Ser Glu Thr Glu Glu Glu
 195 200 205

Glu Glu Thr Lys Asn Pro Lys Gln Lys Ile Ala Gln Thr Arg Arg Pro
 210 215 220

Asp Pro Pro Thr Ala Ala Leu Asn Glu Pro Gln Thr Phe Asp Cys Ala
 225 230 235 240

Leu

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 Leu Asp Glu Met Met Asp Leu Ser Asp Leu Pro Thr Ser Leu Phe Ala
 20 25 30

tgc agc gtc cat gaa gca gtg ttt gag gca cga gag cag aag gaa aga 145
Cys Ser Val His Glu Ala Val Phe Glu Ala Arg Glu Gln Lys Glu Arg
35 40 45

ttt gaa gca ctc ttc acc atc tat gat gac cag gtt act ttt cag ctg 193
 Phe Glu Ala Leu Phe Thr Ile Tyr Asp Asp Gln Val Thr Phe Gln Leu
 50 55 60

ttt aaa agc ttt aga aga gtc aga ata aat ttc agc aaa cct gaa gcg 241
 Phe Lys Ser Phe Arg Arg Val Arg Ile Asn Phe Ser Lys Pro Glu Ala
 65 70 75 80

gca gca aga gcg cga ata gaa ctc cac gaa aca gac ttc aat ggg cag	289	
Ala Ala Arg Ala Arg Ile Glu Leu His Glu Thr Asp Phe Asn Gly Gln		
85	90	95

aag cta aag cta tat ttt gca cag tcc tat ctc ctg ccg ccc cag cct 337
 Lys Leu Lys Leu Tyr Phe Ala Gln Ser Tyr Leu Leu Pro Pro Gln Pro
 100 105 110

gtc aag cag ttc ctc atc tcc cct cca gcc tct ccc cca gtg ggg tgg 385
 Val Lys Gln Phe Leu Ile Ser Pro Pro Ala Ser Pro Pro Val Gly Trp
 115 120 125

aag cag agc gaa gat gcg atg cct gtt ata aat tat gat tta ctc tgt	433	
Lys Gln Ser Glu Asp Ala Met Pro Val Ile Asn Tyr Asp Leu Leu Cys		
130	135	140

gct gtt tcc aaa ttg gga cca gga gag aaa tat gaa ctt cac gcg gga 481
 Ala Val Ser Lys Leu Gly Pro Gly Glu Lys Tyr Glu Leu His Ala Gly
 145 150 155 160

aca gag tcg aca ccc agc gtg gtg gtt cat gtc tgt gaa agt gaa act 529
 Thr Glu Ser Thr Pro Ser Val Val Val His Val Cys Glu Ser Glu Thr
 165 170 175

gaa gag gaa gag aca aaa aac ccc aaa cag aaa att gcc cag aca 577
 Glu Glu Glu Glu Glu Thr Lys Asn Pro Lys Gln Lys Ile Ala Gln Thr
 180 185 190

agg cgc ccc gac cct ccg acc gca gcg ttg aat gag ccc cag acc ttt 625
 Arg Arg Pro Asp Pro Pro Thr Ala Ala Leu Asn Glu Pro Gln Thr Phe
 195 200 205

gat tgc gcg ctg tgaggcctt gggtgtggtg cgaggcggct gccctggtgg 677
Asp Cys Ala Leu
210

gctctggcca tggcgctctg tgcctgcggc cgatgcgttg ctg 720

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<211> 212
<212> PRT
<213> Homo sapiens

<400> 24
Asp Gln Glu Glu Glu Glu Met Ile Phe Gly Glu Asn Glu Asp Asp
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Leu Asp Glu Met Met Asp Leu Ser Asp Leu Pro Thr Ser Leu Phe Ala
20 25 30
Cys Ser Val His Glu Ala Val Phe Glu Ala Arg Glu Gln Lys Glu Arg
35 40 45
Phe Glu Ala Leu Phe Thr Ile Tyr Asp Asp Gln Val Thr Phe Gln Leu
50 55 60
Phe Lys Ser Phe Arg Arg Val Arg Ile Asn Phe Ser Lys Pro Glu Ala
65 70 75 80
Ala Ala Arg Ala Arg Ile Glu Leu His Glu Thr Asp Phe Asn Gly Gln
85 90 95
Lys Leu Lys Leu Tyr Phe Ala Gln Ser Tyr Leu Leu Pro Pro Gln Pro
100 105 110
Val Lys Gln Phe Leu Ile Ser Pro Pro Ala Ser Pro Pro Val Gly Trp
115 120 125
Lys Gln Ser Glu Asp Ala Met Pro Val Ile Asn Tyr Asp Leu Leu Cys
130 135 140
Ala Val Ser Lys Leu Gly Pro Gly Glu Lys Tyr Glu Leu His Ala Gly
145 150 155 160
Thr Glu Ser Thr Pro Ser Val Val His Val Cys Glu Ser Glu Thr
165 170 175
Glu Glu Glu Glu Thr Lys Asn Pro Lys Gln Lys Ile Ala Gln Thr
180 185 190
Arg Arg Pro Asp Pro Pro Thr Ala Ala Leu Asn Glu Pro Gln Thr Phe
195 200 205
Asp Cys Ala Leu
210

<210> 25
<211> 212
<212> PRT
<213> Homo sapiens

<400> 25

Asp Gln Glu Glu Glu Glu Glu Met Ile Phe Gly Glu Asn Glu Asp Asp
 1 5 10 15

Leu Asp Glu Met Met Asp Leu Ser Asp Leu Pro Thr Ser Leu Phe Ala
 20 25 30

Cys Ser Val His Glu Ala Val Phe Glu Ala Arg Glu Gln Lys Glu Arg
 35 40 45

Phe Glu Ala Leu Phe Thr Ile Tyr Asp Asp Gln Val Thr Phe Gln Leu
 50 55 60

Phe Lys Ser Phe Arg Arg Val Arg Ile Asn Phe Ser Lys Pro Glu Ala
 65 70 75 80

Ala Ala Arg Ala Arg Ile Glu Leu His Glu Thr Asp Phe Asn Gly Gln
 85 90 95

Lys Leu Lys Leu Tyr Phe Ala Gln Ser Tyr Leu Leu Pro Pro Gln Pro
 100 105 110

Val Lys Gln Phe Leu Ile Ser Pro Pro Ala Ser Pro Pro Val Gly Trp
 115 120 125

Lys Gln Ser Glu Asp Ala Met Pro Val Ile Asn Tyr Asp Leu Leu Cys
 130 135 140

Ala Val Ser Lys Leu Gly Pro Gly Glu Lys Tyr Glu Leu His Ala Gly
 145 150 155 160

Thr Glu Ser Thr Pro Ser Val Val Val His Val Cys Glu Ser Glu Thr
 165 170 175

Glu Glu Glu Glu Glu Thr Lys Asn Pro Lys Gln Lys Ile Ala Gln Thr
 180 185 190

Arg Arg Pro Asp Pro Pro Thr Ala Ala Leu Asn Glu Pro Gln Thr Phe
 195 200 205

Asp Cys Ala Leu
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<210> 26
 <211> 1039
 <212> DNA
 <213> Homo sapiens

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 cagggacaaa gtgttaagttt ctactggaaa gaggtgacgt caacacctt a gtcattttcc 180
 ctatgctaat taactttgct tggggagaat ggaaaaaaaca gctgaggttt gctccacagc 240
 atcctgtttg gacagcaaat tcctgagtca agtcctgcatt gcttgcaggc agacaggac 300
 aaagtgttaag tttctactgg aaagaggtga cgtcaacacc ttagtcattt tccctatgtc 360
 aattaacttt gcttggggag aatggaaaaa acagctgagg tttgcttcac agctgcttta 420
 tcaacctctc ttgcagcata gtttccactg gtagtaattt cattcagcta ctcagacaac 480

acgctcctcg gccgaatggg acgacccttc ttaagatgga aaatgttaca aaagaaaaag 540
gatgaaggc tggcaata aacagcaatt agactgttagg gaaatttcaa ggcttggg 600
aacctggaaa ccaaagtccg ggtgacatac ttgatccctg gaatttctg aaaacctcaa 660
tcaaagttc actttgggtt attagagaaa acatttgaa atctgtcttgcgtcaataaaa 720
atttaaagg acaaaaagag gaatcatttt gaagtgttagt taaaattttt ttccccagtg 780
acattttattt ggtatgtt cccaaatttctt acttgtatcc cacagtggaa tggagcaaac 840
agaacctaaa acaatcctag gatttcatt tgaaaacttc attattataa tttgagaact 900
ggggatatga aacacttcga tcatttcaa agcactactg aattcaggca aaggatacaa 960
aaacactagc ctttggaaact gagcaatcta gccttggaaa ctgagcaaag aagcattaac 1020
ccatttatgc cagaggttg 1039

<210> 27
<211> 853
<212> DNA
<213> Homo sapiens

<400> 27
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tgaaaatgtt cgaagtgttt catatccccca gttctcaaat tataataatg aagtttcaa 120
atgaaaatcc taggattgtt ttaggttctg tttgctccat tccactgtgg gatacaagta 180
gaaattggga cattcatcca ataaaatgtc actggggaaa aaaattttaa ctacacttca 240
aaatgattcc tcttttgcctt cttaaaattt tttattgacc aagacagatt tcaaaatgtt 300
ttctctaata ccccaaagtg aaactttgat tgaggtttc agggaaattcc agggatcaag 360
tatgtcaccc ggactttggt ttccaggttt cccaaagtct tgaaaatttcc ctacagtcta 420
attgctgtttt attgccacag accttcatcc ttttctttt gtaacattttt ccatcttaag 480
aagggtcgtc ccattcggcc gaggagcgtg ttgtctgagt agctgaatgg aattactacg 540
agtggaaact atgctgcaag agaggttgat aaagcagctg tgaagcaaac ctcagctgtt 600
ttttccatttc tccccaaagca aagttattt gcatagggaa aatgactaag gtgttgacgt 660
cacctctttc cagtagaaac ttacactttg tccctgtcta cctgcaagca tgcaggactt 720
gactcaggaa tttgctgtcc aaacaggatg ctgtggaaagc tgcactttt ttttccccag 780
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cttggaaagg aat 853

SEQUENCE LISTING

<110> WILLIAMS, R. SANDERS
ROTHERMEL, BEVERLY

<120> METHODS AND COMPOSITIONS RELATING TO MUSCLE SELECTIVE
CALCINEURIN INTERACTING PROTEIN (MCIP)

<130> UTSD:674US

<140> UNKNOWN

<141> 2001-02-13

<150> 60/216,601

<151> 2000-07-07

<160> 27

<170> PatentIn Ver. 2.1

<210> 1

<211> 599

<212> DNA

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<400> 1

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tgcttgtgtg gcaaacgatg atgtcttcag cgaaagttag accagggcca aatttgaatc 180
cctcttcaga acatatgaca aggacaccac cttccagtat tttaagagct tcaaacgtgt 240
ccggataaac ttcagcaacc ctttatctgc agccgatgcc aggctgcggc tgcacaagac 300
cgagttcctg gggaggaaa tgaagttgta ttttgctcag actttacaca taggaagttc 360
acacctggct ccgccaatcc cgacaaacag ttccatct cccctccggc ctccctccc 420
gttggctgga aacaagttaga agatgccacc cccgtcataa attacgatct ttttatgcc 480
atctccaagc tggggccagg agagaagtat gaactgcattt cagcgacaga caccactccc 540
agtgtggtgg tccacgtgtg tgagagtgac caagagaatg aggaggaaga ggaagagat 599

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<211> 597

<212> DNA

<213> Mus musculus

<220>

<221> CDS

<222> (1)..(594)

<400> 2

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1 5 10 15	
cac ctg gac ccg cgc gtg ttc gtg gac ggc ctg tgc cgg gcc aaa ttt	96
His Leu Asp Pro Arg Val Phe Val Asp Gly Leu Cys Arg Ala Lys Phe	
20 25 30	
gaa tcc ctc ttc aga aca tat gac aag gac acc acc ttc cag tat ttt	144
Glu Ser Leu Phe Arg Thr Tyr Asp Lys Asp Thr Thr Phe Gln Tyr Phe	
35 40 45	
aag agc ttc aaa cgt gtc ccg ata aac ttc agc aac ccc tta tct gca	192
Lys Ser Phe Lys Arg Val Arg Ile Asn Phe Ser Asn Pro Leu Ser Ala	
50 55 60	
gcc gat gcc agg ctg ccg ctg cac aag acc gag ttc ctg ggg aag gaa	240
Ala Asp Ala Arg Leu Arg Leu His Lys Thr Glu Phe Leu Gly Lys Glu	
65 70 75 80	
atg aag ttg tat ttt gct cag act tta cac ata gga agt tca cac ctg	288
Met Lys Leu Tyr Phe Ala Gln Thr Leu His Ile Gly Ser Ser His Leu	
85 90 95	
gct ccg ccc aat ccc gac aaa cag ttc ctc atc tcc cct ccg gcc tct	336
Ala Pro Pro Asn Pro Asp Lys Gln Phe Leu Ile Ser Pro Pro Ala Ser	
100 105 110	
cct ccc gtt ggc tgg aaa caa gta gaa gat gcc acc ccc gtc ata aat	384
Pro Pro Val Gly Trp Lys Gln Val Glu Asp Ala Thr Pro Val Ile Asn	
115 120 125	
tac gat ctt tta tat gcc atc tcc aag ctg ggg cca gga gag aag tat	432
Tyr Asp Leu Leu Tyr Ala Ile Ser Lys Leu Gly Pro Gly Glu Lys Tyr	
130 135 140	
gaa ctg cat gca gcg aca gac ccc act ccc agt gtg gtg gtc cac gtg	480
Glu Leu His Ala Ala Thr Asp Pro Thr Pro Ser Val Val Val His Val	
145 150 155 160	
tgt gag agt gac caa gag aat gag gag gaa gag gaa gag atg gag aga	528
Cys Glu Ser Asp Gln Glu Asn Glu Glu Glu Glu Glu Met Glu Arg	
165 170 175	
atg aag aga ccc aag ccc aaa atc atc cag aca ccg aga ccg gag tac	576
Met Lys Arg Pro Lys Pro Lys Ile Ile Gln Thr Arg Arg Pro Glu Tyr	
180 185 190	

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Thr Pro Ile His Leu Ser
195

597

<210> 3
<211> 198
<212> PRT
<213> Mus musculus

<400> 3
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His Leu Asp Pro Arg Val Phe Val Asp Gly Leu Cys Arg Ala Lys Phe
20 25 30

Glu Ser Leu Phe Arg Thr Tyr Asp Lys Asp Thr Thr Phe Gln Tyr Phe
35 40 45

Lys Ser Phe Lys Arg Val Arg Ile Asn Phe Ser Asn Pro Leu Ser Ala
50 55 60

Ala Asp Ala Arg Leu Arg Leu His Lys Thr Glu Phe Leu Gly Lys Glu
65 70 75 80

Met Lys Leu Tyr Phe Ala Gln Thr Leu His Ile Gly Ser Ser His Leu
85 90 95

Ala Pro Pro Asn Pro Asp Lys Gln Phe Leu Ile Ser Pro Pro Ala Ser
100 105 110

Pro Pro Val Gly Trp Lys Gln Val Glu Asp Ala Thr Pro Val Ile Asn
115 120 125

Tyr Asp Leu Leu Tyr Ala Ile Ser Lys Leu Gly Pro Gly Glu Lys Tyr
130 135 140

Glu Leu His Ala Ala Thr Asp Pro Thr Pro Ser Val Val Val His Val
145 150 155 160

Cys Glu Ser Asp Gln Glu Asn Glu Glu Glu Glu Glu Met Glu Arg
165 170 175

Met Lys Arg Pro Lys Pro Lys Ile Ile Gln Thr Arg Arg Pro Glu Tyr
180 185 190

Thr Pro Ile His Leu Ser

<210> 4

<211> 198

<212> PRT

<213> Mus musculus

<400> 4

Met Glu Glu Val Asp Leu Gln Asp Leu Pro Ser Ala Thr Ile Ala Cys
1 5 10 15

His Leu Asp Pro Arg Val Phe Val Asp Gly Leu Cys Arg Ala Lys Phe
20 25 30

Glu Ser Leu Phe Arg Thr Tyr Asp Lys Asp Thr Thr Phe Gln Tyr Phe
35 40 45

Lys Ser Phe Lys Arg Val Arg Ile Asn Phe Ser Asn Pro Leu Ser Ala
50 55 60

Ala Asp Ala Arg Leu Arg Leu His Lys Thr Glu Phe Leu Gly Lys Glu
65 70 75 80

Met Lys Leu Tyr Phe Ala Gln Thr Leu His Ile Gly Ser Ser His Leu
85 90 95

Ala Pro Pro Asn Pro Asp Lys Gln Phe Leu Ile Ser Pro Pro Ala Ser
100 105 110

Pro Pro Val Gly Trp Lys Gln Val Glu Asp Ala Thr Pro Val Ile Asn
115 120 125

Tyr Asp Leu Leu Tyr Ala Ile Ser Lys Leu Gly Pro Gly Glu Lys Tyr
130 135 140

Glu Leu His Ala Ala Thr Asp Pro Thr Pro Ser Val Val Val His Val
145 150 155 160

Cys Glu Ser Asp Gln Glu Asn Glu Glu Glu Glu Glu Met Glu Arg
165 170 175

Met Lys Arg Pro Lys Pro Lys Ile Ile Gln Thr Arg Arg Pro Glu Tyr
180 185 190

Thr Pro Ile His Leu Ser
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<213> Mus musculus

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<221> CDS
<222> (1)..(594)

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gtg gca aac gat gat gtc ttc agc gaa agt gag acc agg gcc aaa ttt 96
Val Ala Asn Asp Asp Val Phe Ser Glu Ser Glu Thr Arg Ala Lys Phe
20 25 30

gaa tcc ctc ttc aga aca tat gac aag gac acc acc ttc cag tat ttt 144
Glu Ser Leu Phe Arg Thr Tyr Asp Lys Asp Thr Thr Phe Gln Tyr Phe
35 40 45

aag agc ttc aaa cgt gtc cggtataaac ttc agc aac ccc tta tct gca 192
Lys Ser Phe Lys Arg Val Arg Ile Asn Phe Ser Asn Pro Leu Ser Ala
50 55 60

gcc gat gcc agg ctg cggtctg cac aag acc gag ttc ctg ggg aag gaa 240
Ala Asp Ala Arg Leu Arg Leu His Lys Thr Glu Phe Leu Gly Lys Glu
65 70 75 80

atg aag ttg tat ttt gct cag act tta cac ata gga agt tca cac ctg 288
Met Lys Leu Tyr Phe Ala Gln Thr Leu His Ile Gly Ser Ser His Leu
85 90 95

gct ccg ccc aat ccc gac aaa cag ttc ctc atc tcc cct ccg gcc tct 336
Ala Pro Pro Asn Pro Asp Lys Gln Phe Leu Ile Ser Pro Pro Ala Ser
100 105 110

cct ccc gtt ggc tgg aaa caa gta gaa gat gcc acc ccc gtc ata aat 384
Pro Pro Val Gly Trp Lys Gln Val Glu Asp Ala Thr Pro Val Ile Asn
115 120 125 -

tac gat ctt tta tat gcc atc tcc aag ctg ggg cca gga gag aag tat 432
Tyr Asp Leu Leu Tyr Ala Ile Ser Lys Leu Gly Pro Gly Glu Lys Tyr
130 135 140

gaa ctg cat gca gcg aca gac ccc act ccc agt gtg gtg gtc cac gtg 480
Glu Leu His Ala Ala Thr Asp Pro Thr Pro Ser Val Val Val His Val
145 150 155 160

tgt gag agt gac caa gag aat gag gag gaa gag gaa gag atg gag aga 528
Cys Glu Ser Asp Gln Glu Asn Glu Glu Glu Glu Met Glu Arg
165 170 175

atg aag aga ccc aag ccc aaa atc atc cag aca cgg aga ccg gag tac 576
Met Lys Arg Pro Lys Pro Lys Ile Ile Gln Thr Arg Arg Pro Glu Tyr
180 185 190

aca ccg atc cac ctt agc tga 597
Thr Pro Ile His Leu Ser
195

<210> 6

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20 25 30

Glu Ser Leu Phe Arg Thr Tyr Asp Lys Asp Thr Thr Phe Gln Tyr Phe
35 40 45

Lys Ser Phe Lys Arg Val Arg Ile Asn Phe Ser Asn Pro Leu Ser Ala
50 55 60

Ala Asp Ala Arg Leu Arg Leu His Lys Thr Glu Phe Leu Gly Lys Glu
65 70 75 80

Met Lys Leu Tyr Phe Ala Gln Thr Leu His Ile Gly Ser Ser His Leu
85 90 95

Ala Pro Pro Asn Pro Asp Lys Gln Phe Leu Ile Ser Pro Pro Ala Ser
100 105 110

Pro Pro Val Gly Trp Lys Gln Val Glu Asp Ala Thr Pro Val Ile Asn
115 120 125

Tyr Asp Leu Leu Tyr Ala Ile Ser Lys Leu Gly Pro Gly Glu Lys Tyr

130

135

140

Glu Leu His Ala Ala Thr Asp Pro Thr Pro Ser Val Val Val His Val
 145 150 155 160

Cys Glu Ser Asp Gln Glu Asn Glu Glu Glu Glu Glu Met Glu Arg
 165 170 175

Met Lys Arg Pro Lys Pro Lys Ile Ile Gln Thr Arg Arg Pro Glu Tyr
 180 185 190

Thr Pro Ile His Leu Ser
 195

<210> 7

<211> 198

<212> PRT

<213> Mus musculus

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Met Asp Phe Arg Asp Phe Ser Tyr Asn Phe Ser Ser Leu Ile Ala Cys
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 20 25 30

Glu Ser Leu Phe Arg Thr Tyr Asp Lys Asp Thr Thr Phe Gln Tyr Phe
 35 40 45

Lys Ser Phe Lys Arg Val Arg Ile Asn Phe Ser Asn Pro Leu Ser Ala
 50 55 60

Ala Asp Ala Arg Leu Arg Leu His Lys Thr Glu Phe Leu Gly Lys Glu
 65 70 75 80

Met Lys Leu Tyr Phe Ala Gln Thr Leu His Ile Gly Ser Ser His Leu
 85 90 95

Ala Pro Pro Asn Pro Asp Lys Gln Phe Leu Ile Ser Pro Pro Ala Ser
 100 105 110

Pro Pro Val Gly Trp Lys Gln Val Glu Asp Ala Thr Pro Val Ile Asn
 115 120 125

Tyr Asp Leu Leu Tyr Ala Ile Ser Lys Leu Gly Pro Gly Glu Lys Tyr
 130 135 140

Glu Leu His Ala Ala Thr Asp Pro Thr Pro Ser Val Val Val His Val
145 150 155 160

Cys Glu Ser Asp Gln Glu Asn Glu Glu Glu Glu Glu Met Glu Arg
165 170 175

Met Lys Arg Pro Lys Pro Lys Ile Ile Gln Thr Arg Arg Pro Glu Tyr
180 185 190

Thr Pro Ile His Leu Ser
195

<210> 8

<211> 594

<212> DNA

<213> Mus musculus

<220>

<221> CDS

<222> (1)..(591)

<400> 8

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1 5 10 15

gtg gtg gat gtg gag gtc ttt acc aat cag gag gtt aag gaa aaa ttc 96
Val Val Asp Val Glu Val Phe Thr Asn Gln Glu Val Lys Glu Lys Phe
20 25 30

gag gga ctg ttc cgg acc tat gat gaa tgt gtg acg ttc cag ctg ttt 144
Glu Gly Leu Phe Arg Thr Tyr Asp Glu Cys Val Thr Phe Gln Leu Phe
35 40 45

aag agt ttc cga cgg gtt cga ata aat ttc agc cat ccc aaa tct gca 192
Lys Ser Phe Arg Arg Val Arg Ile Asn Phe Ser His Pro Lys Ser Ala
50 55 60

gcc cgt gcc cgg ata gag ctt cat gag act cag ttc aga ggg aag aag 240
Ala Arg Ala Arg Ile Glu Leu His Glu Thr Gln Phe Arg Gly Lys Lys
65 70 75 80

cta aaa ctc tac ttc gcc cag gtc cag acc cca gag aca gat gga gac 288
Leu Lys Leu Tyr Phe Ala Gln Val Gln Thr Pro Glu Thr Asp Gly Asp
85 90 95

aaa ctg cat ttg gca cct cca cag cct gcc aaa cag ttc ctc atc tca 336
Lys Leu His Leu Ala Pro Pro Gln Pro Ala Lys Gln Phe Leu Ile Ser
100 105 110

ccc cct tca tct cct cct gtt ggc tgg aag cct atc agc gat gcc aca 384
Pro Pro Ser Ser Pro Pro Val Gly Trp Lys Pro Ile Ser Asp Ala Thr
115 120 125

cca gtc ctc aac tat gac ctt ctt tat gct gtg gcc aaa cta gga cca 432
Pro Val Leu Asn Tyr Asp Leu Leu Tyr Ala Val Ala Lys Leu Gly Pro
130 135 140

gga gag aaa tat gag ctg cac gct gga act gag tct aca ccg agc gtc 480
Gly Glu Lys Tyr Glu Leu His Ala Gly Thr Glu Ser Thr Pro Ser Val
145 150 155 160

gtg gtg cat gtg tgt gac agc gac atg gag gag gag gag cca aag 528
Val Val His Val Cys Asp Ser Asp Met Glu Glu Glu Asp Pro Lys
165 170 175

act tcc ccc aag cca aaa atc att cag acc cgg cgt ccg ggc ttg cca 576
Thr Ser Pro Lys Pro Lys Ile Ile Gln Thr Arg Arg Pro Gly Leu Pro
180 185 190

ccc tcc gtg tcc aac tga 594
Pro Ser Val Ser Asn
195

<210> 9

<211> 197

<212> PRT

<213> Mus musculus

<400> 9

Met Pro Ala Pro Ser Met Asp Cys Asp Val Ser Thr Leu Val Ala Cys
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Val Val Asp Val Glu Val Phe Thr Asn Gln Glu Val Lys Glu Lys Phe
20 25 30

Glu Gly Leu Phe Arg Thr Tyr Asp Glu Cys Val Thr Phe Gln Leu Phe
35 40 45

Lys Ser Phe Arg Arg Val Arg Ile Asn Phe Ser His Pro Lys Ser Ala
50 55 60

Ala Arg Ala Arg Ile Glu Leu His Glu Thr Gln Phe Arg Gly Lys Lys

65 70 75 80

Leu Lys Leu Tyr Phe Ala Gln Val Gln Thr Pro Glu Thr Asp Gly Asp
85 90 95

Lys Leu His Leu Ala Pro Pro Gln Pro Ala Lys Gln Phe Leu Ile Ser
100 105 110

Pro Pro Ser Ser Pro Pro Val Gly Trp Lys Pro Ile Ser Asp Ala Thr
115 120 125

Pro Val Leu Asn Tyr Asp Leu Leu Tyr Ala Val Ala Lys Leu Gly Pro
130 135 140

Gly Glu Lys Tyr Glu Leu His Ala Gly Thr Glu Ser Thr Pro Ser Val
145 150 155 160

Val Val His Val Cys Asp Ser Asp Met Glu Glu Glu Asp Pro Lys
165 170 175

Thr Ser Pro Lys Pro Lys Ile Ile Gln Thr Arg Arg Pro Gly Leu Pro
180 185 190

Pro Ser Val Ser Asn
195

<210> 10

<211> 197

<212> PRT

<213> Mus musculus

<400> 10

Met Pro Ala Pro Ser Met Asp Cys Asp Val Ser Thr Leu Val Ala Cys
1 5 10 15

Val Val Asp Val Glu Val Phe Thr Asn Gln Glu Val Lys Glu Lys Phe
20 25 30

Glu Gly Leu Phe Arg Thr Tyr Asp Glu Cys Val Thr Phe Gln Leu Phe
35 40 45

Lys Ser Phe Arg Arg Val Arg Ile Asn Phe Ser His Pro Lys Ser Ala
50 55 60

Ala Arg Ala Arg Ile Glu Leu His Glu Thr Gln Phe Arg Gly Lys Lys
65 70 75 80

Leu Lys Leu Tyr Phe Ala Gln Val Gln Thr Pro Glu Thr Asp Gly Asp
85 90 95

Lys Leu His Leu Ala Pro Pro Gln Pro Ala Lys Gln Phe Leu Ile Ser
100 105 110

Pro Pro Ser Ser Pro Pro Val Gly Trp Lys Pro Ile Ser Asp Ala Thr
115 120 125

Pro Val Leu Asn Tyr Asp Leu Leu Tyr Ala Val Ala Lys Leu Gly Pro
130 135 140

Gly Glu Lys Tyr Glu Leu His Ala Gly Thr Glu Ser Thr Pro Ser Val
145 150 155 160

Val Val His Val Cys Asp Ser Asp Met Glu Glu Glu Asp Pro Lys
165 170 175

Thr Ser Pro Lys Pro Lys Ile Ile Gln Thr Arg Arg Pro Gly Leu Pro
180 185 190

Pro Ser Val Ser Asn
195

<210> 11
<211> 2331
<212> DNA
<213> Homo sapiens

<220>
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<222> (144)..(734)

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aggaacctac agcctcttgg aaaggaatct cactaggggc ttgactgcgt gggctctgttag 120

cgctttcact gtaagaaagc aag atg cat ttt aga aac ttt aac tac agt ttt 173
Met His Phe Arg Asn Phe Asn Tyr Ser Phe
1 5 10

agc tcc ctg att gcc tgt gtg gca aac agt gat atc ttc agc gaa agt 221
Ser Ser Leu Ile Ala Cys Val Ala Asn Ser Asp Ile Phe Ser Glu Ser
15 20 25

gaa acc agg gcc aaa ttt gag tcc ctc ttt agg acg tat gac aag gac	269		
Glu Thr Arg Ala Lys Phe Glu Ser Leu Phe Arg Thr Tyr Asp Lys Asp			
30	35	40	
atc acc ttt cag tat ttt aag agc ttc aaa cga gtc aga ata aac ttc	317		
Ile Thr Phe Gln Tyr Phe Lys Ser Phe Lys Arg Val Arg Ile Asn Phe			
45	50	55	
agc aac ccc ttc tcc gca gca gat gcc agg ctc cag ctg cat aag act	365		
Ser Asn Pro Phe Ser Ala Ala Asp Ala Arg Leu Gln Leu His Lys Thr			
60	65	70	
gag ttt ctg gga aag gaa atg aag tta tat ttt gct cag acc tta cac	413		
Glu Phe Leu Gly Lys Glu Met Lys Leu Tyr Phe Ala Gln Thr Leu His			
75	80	85	90
ata gga agc tca cac ctg gct ccg cca aat cca gac aag cag ttt ctg	461		
Ile Gly Ser Ser His Leu Ala Pro Pro Asn Pro Asp Lys Gln Phe Leu			
95	100	105	
atc tcc cct ccc gcc tct ccg cca gtg gga tgg aaa caa gtg gaa gat	509		
Ile Ser Pro Pro Ala Ser Pro Pro Val Gly Trp Lys Gln Val Glu Asp			
110	115	120	
gcg acc cca gtc ata aac tat gat ctc tta tat gcc atc tcc aag ctg	557		
Ala Thr Pro Val Ile Asn Tyr Asp Leu Leu Tyr Ala Ile Ser Lys Leu			
125	130	135	
ggg cca ggg gaa aag tat gaa ttg cac gca gcg act gac acc act ccc	605		
Gly Pro Gly Glu Lys Tyr Glu Leu His Ala Ala Thr Asp Thr Thr Pro			
140	145	150	
agc gtg gtg gtc cat gta tgt gag agt gat caa gag aag gag gaa gaa	653		
Ser Val Val Val His Val Cys Glu Ser Asp Gln Glu Lys Glu Glu Glu			
155	160	165	170
gag gaa atg gaa aga atg agg aga cct aag cca aaa att atc cag acc	701		
Glu Glu Met Glu Arg Met Arg Arg Pro Lys Pro Lys Ile Ile Gln Thr			
175	180	185	
agg agg ccg gag tac acg ccg atc cac ctc agc tgaactggca cgcgacgagg	754		
Arg Arg Pro Glu Tyr Thr Pro Ile His Leu Ser			
190	195		
acgcattcca aatcatactc acgggaggaa tctttactg tggaggtggc tggcacgac	814		
ttcttcggag gtggcagccg agatcggggt ggcagaaatc ccagttcatg ttgctcagaa	874		

<210> 12

<211> 197

<212> PRT

<213> Homo sapiens

<400> 12

Met His Phe Arg Asn Phe Asn Tyr Ser Phe Ser Ser Leu Ile Ala Cys
1 5 10 15

Val Ala Asn Ser Asp Ile Phe Ser Glu Ser Glu Thr Arg Ala Lys Phe
20 25 30

Glu Ser Leu Phe Arg Thr Tyr Asp Lys Asp Ile Thr Phe Gln Tyr Phe
35 40 45

Lys Ser Phe Lys Arg Val Arg Ile Asn Phe Ser Asn Pro Phe Ser Ala
50 55 60

Ala Asp Ala Arg Leu Gln Leu His Lys Thr Glu Phe Leu Gly Lys Glu
65 70 75 80

Met Lys Leu Tyr Phe Ala Gln Thr Leu His Ile Gly Ser Ser His Leu
85 90 95

Ala Pro Pro Asn Pro Asp Lys Gln Phe Leu Ile Ser Pro Pro Ala Ser
100 105 110

Pro Pro Val Gly Trp Lys Gln Val Glu Asp Ala Thr Pro Val Ile Asn
115 120 125

Tyr Asp Leu Leu Tyr Ala Ile Ser Lys Leu Gly Pro Gly Glu Lys Tyr
130 135 140

Glu Leu His Ala Ala Thr Asp Thr Thr Pro Ser Val Val Val His Val
145 150 155 160

Cys Glu Ser Asp Gln Glu Lys Glu Glu Glu Glu Met Glu Arg Met
165 170 175

Arg Arg Pro Lys Pro Lys Ile Ile Gln Thr Arg Arg Pro Glu Tyr Thr
180 185 190

Pro Ile His Leu Ser
195

<210> 13
<211> 197
<212> PRT
<213> Homo sapiens

<400> 13
Met His Phe Arg Asn Phe Asn Tyr Ser Phe Ser Ser Leu Ile Ala Cys
1 5 10 15

Val Ala Asn Ser Asp Ile Phe Ser Glu Ser Glu Thr Arg Ala Lys Phe
20 25 30

Glu Ser Leu Phe Arg Thr Tyr Asp Lys Asp Ile Thr Phe Gln Tyr Phe
35 40 45

Lys Ser Phe Lys Arg Val Arg Ile Asn Phe Ser Asn Pro Phe Ser Ala
50 55 60

Ala Asp Ala Arg Leu Gln Leu His Lys Thr Glu Phe Leu Gly Lys Glu
65 70 75 80

Met Lys Leu Tyr Phe Ala Gln Thr Leu His Ile Gly Ser Ser His Leu
85 90 95

Ala Pro Pro Asn Pro Asp Lys Gln Phe Leu Ile Ser Pro Pro Ala Ser
100 105 110

Pro Pro Val Gly Trp Lys Gln Val Glu Asp Ala Thr Pro Val Ile Asn
115 120 125

Tyr Asp Leu Leu Tyr Ala Ile Ser Lys Leu Gly Pro Gly Glu Lys Tyr
130 135 140

Glu Leu His Ala Ala Thr Asp Thr Thr Pro Ser Val Val Val His Val
145 150 155 160

Cys Glu Ser Asp Gln Glu Lys Glu Glu Glu Glu Met Glu Arg Met
165 170 175

Arg Arg Pro Lys Pro Lys Ile Ile Gln Thr Arg Arg Pro Glu Tyr Thr
180 185 190

Pro Ile His Leu Ser
195

<210> 14
<211> 2212
<212> DNA
<213> Homo sapiens

<220>
<221> CDS
<222> (25)..(615)

<400> 14
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Met Glu Glu Val Asp Leu Gln Asp Leu
1 5

ccc agc gcc acc atc gcc tgt cac ctg gac ccg cgc gtg ttc gtg gac 99
Pro Ser Ala Thr Ile Ala Cys His Leu Asp Pro Arg Val Phe Val Asp
10 15 20 25

ggc ctg tgc cgg gcc aaa ttt gag tcc ctc ttt agg acg tat gac aag 147
Gly Leu Cys Arg Ala Lys Phe Glu Ser Leu Phe Arg Thr Tyr Asp Lys
30 35 40

gac atc acc ttt cag tat ttt aag agc ttc aaa cga gtc aga ata aac 195
Asp Ile Thr Phe Gln Tyr Phe Lys Ser Phe Lys Arg Val Arg Ile Asn
45 50 55

ttc agc aac ccc ttc tcc gca gca gat gcc agg ctc cag ctg cat aag 243
Phe Ser Asn Pro Phe Ser Ala Ala Asp Ala Arg Leu Gln Leu His Lys
60 65 70

act gag ttt ctg gga aag gaa atg aag tta tat ttt gct cag acc tta 291
Thr Glu Phe Leu Gly Lys Glu Met Lys Leu Tyr Phe Ala Gln Thr Leu
75 80 85

cac ata gga agc tca cac ctg gct ccg cca aat cca gac aag cag ttt 339
His Ile Gly Ser Ser His Leu Ala Pro Pro Asn Pro Asp Lys Gln Phe
90 95 100 105

ctg atc tcc cct ccc gcc tct ccg cca gtg gga tgg aaa caa gtg gaa 387
Leu Ile Ser Pro Pro Ala Ser Pro Pro Val Gly Trp Lys Gln Val Glu
110 115 120

gat gcg acc cca gtc ata aac tat gat ctc tta tat gcc atc tcc aag 435
Asp Ala Thr Pro Val Ile Asn Tyr Asp Leu Leu Tyr Ala Ile Ser Lys
125 130 135

ctg ggg cca ggg gaa aag tat gaa ttg cac gca gcg act gac acc act 483
Leu Gly Pro Gly Glu Lys Tyr Glu Leu His Ala Ala Thr Asp Thr Thr

140

145

150

ccc agc gtg gtg gtc cat gta tgt gag agt gat caa gag aag gag gaa 531
 Pro Ser Val Val Val His Val Cys Glu Ser Asp Gln Glu Lys Glu Glu
 155 160 165

gaa gag gaa atg gaa aga atg agg aga cct aag cca aaa att atc cag 579
 Glu Glu Glu Met Glu Arg Met Arg Arg Pro Lys Pro Lys Ile Ile Gln
 170 175 180 185

acc agg agg ccg gag tac acg ccg atc cac ctc agc tgaactggca 625
 Thr Arg Arg Pro Glu Tyr Thr Pro Ile His Leu Ser
 190 195

cgcgacgagg acgcattcca aatcatactc acgggaggaa tctttactg tggaggtggc 685
 tggtcacgac ttctcggag gtggcagccg agatcggtt ggcagaaatc ccagttcatg 745
 ttgctcagaa gagaatcaag gccgtgtccc cttgttctaa tgctgcacac cagttactgt 805
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taaatgcttt gattgttcat atcaagaaat tgattgaacg ttctcaaacc ctgtttacgg 2065
tacttggtaa gaggagccg gtttggaga gaccattgca tcgctgtcca agtgttctt 2125
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aataaatggg cacagtatgc tccttac 2212

<210> 15

<211> 197

<212> PRT

<213> Homo sapiens

<400> 15

Met Glu Glu Val Asp Leu Gln Asp Leu Pro Ser Ala Thr Ile Ala Cys
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His Leu Asp Pro Arg Val Phe Val Asp Gly Leu Cys Arg Ala Lys Phe
20 25 30

Glu Ser Leu Phe Arg Thr Tyr Asp Lys Asp Ile Thr Phe Gln Tyr Phe
35 40 45

Lys Ser Phe Lys Arg Val Arg Ile Asn Phe Ser Asn Pro Phe Ser Ala
50 55 60

Ala Asp Ala Arg Leu Gln Leu His Lys Thr Glu Phe Leu Gly Lys Glu
65 70 75 80

Met Lys Leu Tyr Phe Ala Gln Thr Leu His Ile Gly Ser Ser His Leu
85 90 95

Ala Pro Pro Asn Pro Asp Lys Gln Phe Leu Ile Ser Pro Pro Ala Ser
100 105 110

Pro Pro Val Gly Trp Lys Gln Val Glu Asp Ala Thr Pro Val Ile Asn
115 120 125

Tyr Asp Leu Leu Tyr Ala Ile Ser Lys Leu Gly Pro Gly Glu Lys Tyr
130 135 140

Glu Leu His Ala Ala Thr Asp Thr Thr Pro Ser Val Val Val His Val
145 150 155 160

Cys Glu Ser Asp Gln Glu Lys Glu Glu Glu Met Glu Arg Met
165 170 175

Arg Arg Pro Lys Pro Lys Ile Ile Gln Thr Arg Arg Pro Glu Tyr Thr
180 185 190

Pro Ile His Leu Ser
195

<210> 16
<211> 197
<212> PRT
<213> Homo sapiens

<400> 16
Met Glu Glu Val Asp Leu Gln Asp Leu Pro Ser Ala Thr Ile Ala Cys
1 5 10 15

His Leu Asp Pro Arg Val Phe Val Asp Gly Leu Cys Arg Ala Lys Phe
20 25 30

Glu Ser Leu Phe Arg Thr Tyr Asp Lys Asp Ile Thr Phe Gln Tyr Phe
35 40 45

Lys Ser Phe Lys Arg Val Arg Ile Asn Phe Ser Asn Pro Phe Ser Ala
50 55 60

Ala Asp Ala Arg Leu Gln Leu His Lys Thr Glu Phe Leu Gly Lys Glu
65 70 75 80

Met Lys Leu Tyr Phe Ala Gln Thr Leu His Ile Gly Ser Ser His Leu
85 90 95

Ala Pro Pro Asn Pro Asp Lys Gln Phe Leu Ile Ser Pro Pro Ala Ser
100 105 110

Pro Pro Val Gly Trp Lys Gln Val Glu Asp Ala Thr Pro Val Ile Asn

115 120 125
Tyr Asp Leu Leu Tyr Ala Ile Ser Lys Leu Gly Pro Gly Glu Lys Tyr
130 135 140

Glu Leu His Ala Ala Thr Asp Thr Thr Pro Ser Val Val Val His Val
145 150 155 160

Cys Glu Ser Asp Gln Glu Lys Glu Glu Glu Glu Met Glu Arg Met
165 170 175

Arg Arg Pro Lys Pro Lys Ile Ile Gln Thr Arg Arg Pro Glu Tyr Thr
180 185 190

Pro Ile His Leu Ser
195

<210> 17
<211> 3184
<212> DNA
<213> Homo sapiens

<220>
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<222> (205)..(780)

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cgagcctcca gccgtcctca gagcaaggca gcaccgaggc ctggccacag caatatccat 120
ctggaagctc ttcccttcac tcccaactct gaggttgccct aactctttat taaaaattca 180
gaagggggaa tgccagcccc tagc atg gac tgt gat gtt tcc act ctg gtt 231
Met Asp Cys Asp Val Ser Thr Leu Val
1 5

gcc tgt gtg gtg gat gtc gag gtc ttt acc aat cag gag gtt aag gaa 279
Ala Cys Val Val Asp Val Glu Val Phe Thr Asn Gln Glu Val Lys Glu
10 15 20 25

aaa ttt ggg gga ctg ttt cgg act tat gat gac tgt gtg acg ttc cag 327
Lys Phe Gly Gly Leu Phe Arg Thr Tyr Asp Asp Cys Val Thr Phe Gln
30 35 40

cta ttt aag agt ttc aga cgt gtc cgt ata aac ttc agc aat cct aaa 375
Leu Phe Lys Ser Phe Arg Arg Val Arg Ile Asn Phe Ser Asn Pro Lys

45

50

55

tct gca gcc cga gct agg ata gag ctt cat gaa acc caa ttc aga ggg 423
 Ser Ala Ala Arg Ala Arg Ile Glu Leu His Glu Thr Gln Phe Arg Gly
 60 65 70

aaa aaa tta aag ctc tac ttt gca cag gtt cag act cca gag aca gat 471
 Lys Lys Leu Lys Leu Tyr Phe Ala Gln Val Gln Thr Pro Glu Thr Asp
 75 80 85

gga gac aaa ctg cac ttg gct cca ccc cag cct gcc aaa cag ttt ctc 519
 Gly Asp Lys Leu His Leu Ala Pro Pro Gln Pro Ala Lys Gln Phe Leu
 90 95 100 105

atc tcg ccc cct tcc tcc cca cct gtt agc tgg cag ccc atc aac gat 567
 Ile Ser Pro Pro Ser Ser Pro Pro Val Ser Trp Gln Pro Ile Asn Asp
 110 115 120

gcc acg cca gtc ctc aac tat gac ctc ctc tat gct gtg gcc aaa cta 615
 Ala Thr Pro Val Leu Asn Tyr Asp Leu Leu Tyr Ala Val Ala Lys Leu
 125 130 135

gga cca gga gag aag tat gag ctc cat gca ggg act gag tcc acc cca 663
 Gly Pro Gly Glu Lys Tyr Glu Leu His Ala Gly Thr Glu Ser Thr Pro
 140 145 150

agt gtc gtc gtg cac gtg tgc gac agt gac ata gag gaa gaa gag gac 711
 Ser Val Val Val His Val Cys Asp Ser Asp Ile Glu Glu Glu Glu Asp
 155 160 165

cca aag act tcc cca aag cca aaa atc atc caa act cgg cgt cct ggc 759
 Pro Lys Thr Ser Pro Lys Pro Lys Ile Ile Gln Thr Arg Arg Pro Gly
 170 175 180 185

ctg cca ccc tcc gtg tcc aac tgagctgcct gctccttctc gataatagcc 810
 Leu Pro Pro Ser Val Ser Asn
 190

gtctccttctt tatcatgctt tttccccctg ttgtttgtca aaaaaaatttgc cttttttttt 870

cctgggtgtt tggttgtttg agattccttc cttgttatca agcctctcgg acaaaaaggc 930

tagaaaaagg tgatatgtct cctgatcata tcataccat taagtataac ccattattta 990

gaaggttcta gggaaaaaaag tagtattttc ttattaaaca atcagcacag cctatatctt 1050

tgttctctca tggatcca agccagagac atcggttaca aatagcacact gtgttgg 1110

tgaggtgttt cagtccaggc cctgatgtgt gtgcgttggc ctctcctggc cacttaata 1170
ggaccatatg taaacttgac tttgactgca tgagatatcc ctatctggtc tcactcagtc 1230
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ttatgaatgc cttcatatac taatacagat actctgataa tattacactc taataaggat 1770
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gggatgaagc taaatccccaa gaatgcagca gcgcgtgagc atgttaaaat ggggaaggat 1950
gatagctaca tgtatgccgg tcctactcac gcgcacacccg tggctcaaa aaagttactt 2010
gttttgtta cgtgtgattt tcctatttct ctagccaaa gtgcattaca gaagatacac 2070
ctatagaacc attaccttct gctatgtgtg ccaggcgtca tctactcctg tacattaatg 2130
gattacttta gatgcaaatg cagattacaa tggagtgggg aagtacttcc attacccaag 2190
cctcagaaaa acacacaaga acaataacac agcaaaacaga ttgagggatt gttgtggttt 2250
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tagtggaga aatagtagct ccgctattca gatgcagagc actgcagcat ccagccttc 2610
aaagctgact cttctcaatc atctgtgggt catttgactt gatttttaa gctaccctga 2670
attccagaa tgcagggtct aaagaaatct agatgagaga aagtatttga aaatgattt 2730
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cattctgtgt agtcataaaa gaaacacaat gaagtgtatg gcctctggag ttagtcttag 2850
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gttgggtttg gggagggggg aaaagaggggg ctttcctag gagaacgata agaaatggaa 2970
agactccttg aagtgttgca agggAACCTC ctgcactgt gaaagtcaga atgcctcag 3030
cattccatg acgcacatca tgcaaatttc tttagcacta ttttaaggaa gaaaacttta 3090
acaatgaagg ggaaggggaa gatttccacc aactgaatca tttgtgcacg tgtatagctc 3150
aaagagctta gacttcaaattt atatctggtg aatg 3184

<210> 18
<211> 192
<212> PRT
<213> Homo sapiens

<400> 18
Met Asp Cys Asp Val Ser Thr Leu Val Ala Cys Val Val Asp Val Glu
1 5 10 15
Val Phe Thr Asn Gln Glu Val Lys Glu Lys Phe Gly Gly Leu Phe Arg
20 25 30
Thr Tyr Asp Asp Cys Val Thr Phe Gln Leu Phe Lys Ser Phe Arg Arg
35 40 45
Val Arg Ile Asn Phe Ser Asn Pro Lys Ser Ala Ala Arg Ala Arg Ile
50 55 60
Glu Leu His Glu Thr Gln Phe Arg Gly Lys Lys Leu Lys Leu Tyr Phe
65 70 75 80
Ala Gln Val Gln Thr Pro Glu Thr Asp Gly Asp Lys Leu His Leu Ala
85 90 95
Pro Pro Gln Pro Ala Lys Gln Phe Leu Ile Ser Pro Pro Ser Ser Pro

100

105

110

Pro Val Ser Trp Gln Pro Ile Asn Asp Ala Thr Pro Val Leu Asn Tyr
115 120 125

Asp Leu Leu Tyr Ala Val Ala Lys Leu Gly Pro Gly Glu Lys Tyr Glu
130 135 140

Leu His Ala Gly Thr Glu Ser Thr Pro Ser Val Val Val His Val Cys
145 150 155 160

Asp Ser Asp Ile Glu Glu Glu Asp Pro Lys Thr Ser Pro Lys Pro
165 170 175

Lys Ile Ile Gln Thr Arg Arg Pro Gly Leu Pro Pro Ser Val Ser Asn
180 185 190

<210> 19

<211> 192

<212> PRT

<213> Homo sapiens

<400> 19

Met Asp Cys Asp Val Ser Thr Leu Val Ala Cys Val Val Asp Val Glu
1 5 10 15

Val Phe Thr Asn Gln Glu Val Lys Glu Lys Phe Gly Gly Leu Phe Arg
20 25 30

Thr Tyr Asp Asp Cys Val Thr Phe Gln Leu Phe Lys Ser Phe Arg Arg
35 40 45

Val Arg Ile Asn Phe Ser Asn Pro Lys Ser Ala Ala Arg Ala Arg Ile
50 55 60

Glu Leu His Glu Thr Gln Phe Arg Gly Lys Lys Leu Lys Leu Tyr Phe
65 70 75 80

Ala Gln Val Gln Thr Pro Glu Thr Asp Gly Asp Lys Leu His Leu Ala
85 90 95

Pro Pro Gln Pro Ala Lys Gln Phe Leu Ile Ser Pro Pro Ser Ser Pro
100 105 110

Pro Val Ser Trp Gln Pro Ile Asn Asp Ala Thr Pro Val Leu Asn Tyr
115 120 125

Asp Leu Leu Tyr Ala Val Ala Lys Leu Gly Pro Gly Glu Lys Tyr Glu
130 135 140

Leu His Ala Gly Thr Glu Ser Thr Pro Ser Val Val Val His Val Cys
145 150 155 160

Asp Ser Asp Ile Glu Glu Glu Asp Pro Lys Thr Ser Pro Lys Pro
165 170 175

Lys Ile Ile Gln Thr Arg Arg Pro Gly Leu Pro Pro Ser Val Ser Asn
180 185 190

<210> 20

<211> 828

<212> DNA

<213> Homo sapiens

<220>

<221> CDS

<222> (23)..(745)

<400> 20

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Met Leu Arg Asp Thr Met Lys Ser Trp Asn
1 5 10

gat agc cag tca gat ctg tgt agc act gac caa gaa gag gaa gag 100
Asp Ser Gln Ser Asp Leu Cys Ser Thr Asp Gln Glu Glu Glu Glu
15 20 25

atg att ttt ggt gaa aat gaa gat gat ttg gat gag atg atg gat tta 148
Met Ile Phe Gly Glu Asn Glu Asp Asp Leu Asp Glu Met Met Asp Leu
30 35 40

agt gat ctg cct acc tca ctt ttt gct tgc agc gtc cat gaa gca gtg 196
Ser Asp Leu Pro Thr Ser Leu Phe Ala Cys Ser Val His Glu Ala Val
45 50 55

ttt gag gca cga gag cag aag gaa aga ttt gaa gca ctc ttc acc atc 244
Phe Glu Ala Arg Glu Gln Lys Glu Arg Phe Glu Ala Leu Phe Thr Ile
60 65 70

tat gat gac cag gtt act ttt cag ctg ttt aaa agc ttt aga aga gtc 292

Tyr Asp Asp Gln Val Thr Phe Gln Leu Phe Lys Ser Phe Arg Arg Val			
75	80	85	90
aga ata aat ttc agc aaa cct gaa gcg gca gca aga gcg cga ata gaa			340
Arg Ile Asn Phe Ser Lys Pro Glu Ala Ala Ala Arg Ala Arg Ile Glu			
95	100	105	
ctc cac gaa aca gac ttc aat ggg cag aag cta aag cta tat ttt gca			388
Leu His Glu Thr Asp Phe Asn Gly Gln Lys Leu Lys Leu Tyr Phe Ala			
110	115	120	
cag gtg cag atg tcc ggc gaa gtg cgg gac aag tcc tat ctc ctg ccg			436
Gln Val Gln Met Ser Gly Glu Val Arg Asp Lys Ser Tyr Leu Leu Pro			
125	130	135	
ccc cag cct gtc aag cag ttc ctc atc tcc cct cca gcc tct ccc cca			484
Pro Gln Pro Val Lys Gln Phe Leu Ile Ser Pro Pro Ala Ser Pro Pro			
140	145	150	
gtg ggg tgg aag cag agc gaa gat gcg atg cct gtt ata aat tat gat			532
Val Gly Trp Lys Gln Ser Glu Asp Ala Met Pro Val Ile Asn Tyr Asp			
155	160	165	170
tta ctc tgt gct gtt tcc aaa ttg gga cca gga gag aaa tat gaa ctt			580
Leu Leu Cys Ala Val Ser Lys Leu Gly Pro Gly Glu Lys Tyr Glu Leu			
175	180	185	
cac gcg gga aca gag tcg aca ccc agc gtg gtg gtt cat gtc tgt gaa			628
His Ala Gly Thr Glu Ser Thr Pro Ser Val Val Val His Val Cys Glu			
190	195	200	
agt gaa act gaa gag gaa gag aca aaa aac ccc aaa cag aaa att			676
Ser Glu Thr Glu Glu Glu Glu Thr Lys Asn Pro Lys Gln Lys Ile			
205	210	215	
gcc cag aca agg cgc ccc gac cct ccg acc gca gcg ttg aat gag ccc			724
Ala Gln Thr Arg Arg Pro Asp Pro Pro Thr Ala Ala Leu Asn Glu Pro			
220	225	230	
cag acc ttt gat tgc gcg ctg tgaggccctt gggtgtggtg cgaggcggct			775
Gln Thr Phe Asp Cys Ala Leu			
235	240		
gccctggtgg gctctggcca tggcgctctg tgcctgcggc cgatgcgttg ctg			828

<210> 21

<211> 241

<212> PRT

<213> Homo sapiens

<400> 21

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Cys Ser Thr Asp Gln Glu Glu Glu Glu Met Ile Phe Gly Glu Asn
20 25 30

Glu Asp Asp Leu Asp Glu Met Met Asp Leu Ser Asp Leu Pro Thr Ser
35 40 45

Leu Phe Ala Cys Ser Val His Glu Ala Val Phe Glu Ala Arg Glu Gln
50 55 60

Lys Glu Arg Phe Glu Ala Leu Phe Thr Ile Tyr Asp Asp Gln Val Thr
65 70 75 80

Phe Gln Leu Phe Lys Ser Phe Arg Arg Val Arg Ile Asn Phe Ser Lys
85 90 95

Pro Glu Ala Ala Ala Arg Ala Arg Ile Glu Leu His Glu Thr Asp Phe
100 105 110

Asn Gly Gln Lys Leu Lys Leu Tyr Phe Ala Gln Val Gln Met Ser Gly
115 120 125

Glu Val Arg Asp Lys Ser Tyr Leu Leu Pro Pro Gln Pro Val Lys Gln
130 135 140

Phe Leu Ile Ser Pro Pro Ala Ser Pro Pro Val Gly Trp Lys Gln Ser
145 150 155 160

Glu Asp Ala Met Pro Val Ile Asn Tyr Asp Leu Leu Cys Ala Val Ser
165 170 175

Lys Leu Gly Pro Gly Glu Lys Tyr Glu Leu His Ala Gly Thr Glu Ser
180 185 190

Thr Pro Ser Val Val Val His Val Cys Glu Ser Glu Thr Glu Glu Glu
195 200 205

Glu Glu Thr Lys Asn Pro Lys Gln Lys Ile Ala Gln Thr Arg Arg Pro
210 215 220

Asp Pro Pro Thr Ala Ala Leu Asn Glu Pro Gln Thr Phe Asp Cys Ala
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Leu

<210> 22

<211> 241

<212> PRT

<213> Homo sapiens

<400> 22

Met Leu Arg Asp Thr Met Lys Ser Trp Asn Asp Ser Gln Ser Asp Leu
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Cys Ser Thr Asp Gln Glu Glu Glu Glu Met Ile Phe Gly Glu Asn
20 25 30

Glu Asp Asp Leu Asp Glu Met Met Asp Leu Ser Asp Leu Pro Thr Ser
35 40 45

Leu Phe Ala Cys Ser Val His Glu Ala Val Phe Glu Ala Arg Glu Gln
50 55 60

Lys Glu Arg Phe Glu Ala Leu Phe Thr Ile Tyr Asp Asp Gln Val Thr
65 70 75 80

Phe Gln Leu Phe Lys Ser Phe Arg Arg Val Arg Ile Asn Phe Ser Lys
85 90 95

Pro Glu Ala Ala Ala Arg Ala Arg Ile Glu Leu His Glu Thr Asp Phe
100 105 110

Asn Gly Gln Lys Leu Lys Leu Tyr Phe Ala Gln Val Gln Met Ser Gly
115 120 125

Glu Val Arg Asp Lys Ser Tyr Leu Leu Pro Pro Gln Pro Val Lys Gln
130 135 140

Phe Leu Ile Ser Pro Pro Ala Ser Pro Pro Val Gly Trp Lys Gln Ser
145 150 155 160

Glu Asp Ala Met Pro Val Ile Asn Tyr Asp Leu Leu Cys Ala Val Ser
165 170 175

Lys Leu Gly Pro Gly Glu Lys Tyr Glu Leu His Ala Gly Thr Glu Ser
180 185 190

Thr Pro Ser Val Val Val His Val Cys Glu Ser Glu Thr Glu Glu Glu
195 200 205

Glu Glu Thr Lys Asn Pro Lys Gln Lys Ile Ala Gln Thr Arg Arg Pro
210 215 220

Asp Pro Pro Thr Ala Ala Leu Asn Glu Pro Gln Thr Phe Asp Cys Ala
225 230 235 240

Leu

<210> 23

<211> 720

<212> DNA

<213> Homo sapiens

<220>

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<400> 23

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Leu Asp Glu Met Met Asp Leu Ser Asp Leu Pro Thr Ser Leu Phe Ala
20 25 30

tgc agc gtc cat gaa gca gtg ttt gag gca cga gag cag aag gaa aga 145
Cys Ser Val His Glu Ala Val Phe Glu Ala Arg Glu Gln Lys Glu Arg
35 40 45

ttt gaa gca ctc ttc acc atc tat gat gac cag gtt act ttt cag ctg 193
Phe Glu Ala Leu Phe Thr Ile Tyr Asp Asp Gln Val Thr Phe Gln Leu
50 55 60

ttt aaa agc ttt aga aga gtc aga ata aat ttc agc aaa cct gaa gcg 241
Phe Lys Ser Phe Arg Arg Val Arg Ile Asn Phe Ser Lys Pro Glu Ala
65 70 75 80

gca gca aga gcg cga ata gaa ctc cac gaa aca gac ttc aat ggg cag 289
Ala Ala Arg Ala Arg Ile Glu Leu His Glu Thr Asp Phe Asn Gly Gln
85 90 95

aag cta aag cta tat ttt gca cag tcc tat ctc ctg ccg ccc cag cct 337

Lys	Leu	Lys	Leu	Tyr	Phe	Ala	Gln	Ser	Tyr	Leu	Leu	Pro	Pro	Gln	Pro	
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gtc aag cag ttc ctc atc tcc cct cca gcc tct ccc cca gtg ggg tgg															385	
Val	Lys	Gln	Phe	Leu	Ile	Ser	Pro	Pro	Ala	Ser	Pro	Pro	Val	Gly	Trp	
115													120		125	
aag cag agc gaa gat gcg atg cct gtt ata aat tat gat tta ctc tgt															433	
Lys	Gln	Ser	Glu	Asp	Ala	Met	Pro	Val	Ile	Asn	Tyr	Asp	Leu	Leu	Cys	
130													135		140	
gct gtt tcc aaa ttg gga cca gga gag aaa tat gaa ctt cac gcg gga															481	
Ala	Val	Ser	Lys	Leu	Gly	Pro	Gly	Glu	Lys	Tyr	Glu	Leu	His	Ala	Gly	
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aca gag tcg aca ccc agc gtg gtg gtt cat gtc tgt gaa agt gaa act															529	
Thr	Glu	Ser	Thr	Pro	Ser	Val	Val	Val	His	Val	Cys	Glu	Ser	Glu	Thr	
165													170		175	
gaa gag gaa gag aca aaa aac ccc aaa cag aaa att gcc cag aca															577	
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180													185		190	
agg cgc ccc gac cct ccg acc gca gcg ttg aat gag ccc cag acc ttt															625	
Arg	Arg	Pro	Asp	Pro	Pro	Thr	Ala	Ala	Leu	Asn	Glu	Pro	Gln	Thr	Phe	
195													200		205	
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Leu Asp Glu Met Met Asp Leu Ser Asp Leu Pro Thr Ser Leu Phe Ala																
20													25		30	
Cys Ser Val His Glu Ala Val Phe Glu Ala Arg Glu Gln Lys Glu Arg																
35													40		45	

Phe Glu Ala Leu Phe Thr Ile Tyr Asp Asp Gln Val Thr Phe Gln Leu
50 55 60

Phe Lys Ser Phe Arg Arg Val Arg Ile Asn Phe Ser Lys Pro Glu Ala
65 70 75 80

Ala Ala Arg Ala Arg Ile Glu Leu His Glu Thr Asp Phe Asn Gly Gln
85 90 95

Lys Leu Lys Leu Tyr Phe Ala Gln Ser Tyr Leu Leu Pro Pro Gln Pro
100 105 110

Val Lys Gln Phe Leu Ile Ser Pro Pro Ala Ser Pro Pro Val Gly Trp
115 120 125

Lys Gln Ser Glu Asp Ala Met Pro Val Ile Asn Tyr Asp Leu Leu Cys
130 135 140

Ala Val Ser Lys Leu Gly Pro Gly Glu Lys Tyr Glu Leu His Ala Gly
145 150 155 160

Thr Glu Ser Thr Pro Ser Val Val His Val Cys Glu Ser Glu Thr
165 170 175

Glu Glu Glu Glu Glu Thr Lys Asn Pro Lys Gln Lys Ile Ala Gln Thr
180 185 190

Arg Arg Pro Asp Pro Pro Thr Ala Ala Leu Asn Glu Pro Gln Thr Phe
195 200 205

Asp Cys Ala Leu
210

<210> 25

<211> 212

<212> PRT

<213> Homo sapiens

<400> 25

Asp Gln Glu Glu Glu Glu Met Ile Phe Gly Glu Asn Glu Asp Asp
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Leu Asp Glu Met Met Asp Leu Ser Asp Leu Pro Thr Ser Leu Phe Ala
20 25 30

Cys Ser Val His Glu Ala Val Phe Glu Ala Arg Glu Gln Lys Glu Arg
35 40 45

Phe Glu Ala Leu Phe Thr Ile Tyr Asp Asp Gln Val Thr Phe Gln Leu
50 55 60

Phe Lys Ser Phe Arg Arg Val Arg Ile Asn Phe Ser Lys Pro Glu Ala
65 70 75 80

Ala Ala Arg Ala Arg Ile Glu Leu His Glu Thr Asp Phe Asn Gly Gln
85 90 95

Lys Leu Lys Leu Tyr Phe Ala Gln Ser Tyr Leu Leu Pro Pro Gln Pro
100 105 110

Val Lys Gln Phe Leu Ile Ser Pro Pro Ala Ser Pro Pro Val Gly Trp
115 120 125

Lys Gln Ser Glu Asp Ala Met Pro Val Ile Asn Tyr Asp Leu Leu Cys
130 135 140

Ala Val Ser Lys Leu Gly Pro Gly Glu Lys Tyr Glu Leu His Ala Gly
145 150 155 160

Thr Glu Ser Thr Pro Ser Val Val Val His Val Cys Glu Ser Glu Thr
165 170 175

Glu Glu Glu Glu Glu Thr Lys Asn Pro Lys Gln Lys Ile Ala Gln Thr
180 185 190

Arg Arg Pro Asp Pro Pro Thr Ala Ala Leu Asn Glu Pro Gln Thr Phe
195 200 205

Asp Cys Ala Leu
210

<210> 26
<211> 1039
<212> DNA
<213> Homo sapiens

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cagggacaaa gtgtaagttt ctactggaaa gaggtgacgt caacacctta gtcattttcc 180
ctatgctaatt taactttgct tggggagaat ggaaaaaaaaaca gctgaggttt gctccacagc 240
atcctgtttg gacagcaaatt tcctgagtca agtcctgcatt gcttgcaggc agacagggac 300

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aattaacttt gcttggggag aatggaaaaa acagctgagg tttgcttcac agctgctta 420
tcaacctctc ttgcagcata gtttccactg gtagtaattc cattcagcta ctcagacaac 480
acgctcctcg gccgaatggg acgacccttc ttaagatgga aaatgttaca aaagaaaaag 540
gatgaaggta tttggcaata aacagcaatt agactgttagg gaaatttcaa ggctttggga 600
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tcaaagttc actttgggtt attagagaaa acattttgaa atctgtcttgcgtcaataaaa 720
attttaaagg acaaaaagag gaatcattttt gaagtgttagt taaaattttt ttccccagtg 780
acattttattt ggtgaatgt cccaaatttct acttgttatcc cacagtggaa tggagcaaac 840
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<210> 27

<211> 853

<212> DNA

<213> Homo sapiens

<400> 27

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atgaaaatcc taggattttt tttaggttctg tttgctccat tccactgtgg gatacaagta 180
gaaattggga cattcatcca ataaaatgtc actggggaaa aaaattttaa ctacacttca 240
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attgctgtttt attgccacag accttcatcc tttttctttt gtaacattttt ccatcttaag 480
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gactcaggaa ttgtgtgtcc aaacaggatg ctgtggaaagc tgcactttt ttttccccag 780
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cttggaaagg aat 853